

SEQUENCE LISTING

<110> Sagami Chemical Research Center,

Protegene Inc.

<120> Human proteins having hydrophobic domains and DNAs encoding these
proteins

<130> 661924

<150> JP 11-178065

<151> 1999-06-24

<160> 24

<210> 1

<211> 238

<212> PRT

<213> Homo sapiens

<400> 1

Met Ile Leu Leu Val Ile Leu Ala Phe Tyr Leu Trp Gln Val Asp Met

1

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10

15

Leu Ser Glu Ile Asn Ile Ala Pro Arg Ile Leu Thr Asn Phe Thr Gly

20

25

30

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Val Met Pro Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu Lys Thr
35 40 45

Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu Gln Val
50 55 60

Ser Asn Glu Pro Gly Asn Arg Tyr Asn Leu Gln Leu Ile Asn Ala Leu
65 70 75 80

Val Leu Tyr Val Gly Thr Gln Ala Ile Ala His Ile His Asn Lys Gly
85 90 95

Ser Thr Pro Ser Met Ser Thr Ile Thr His Ser Ala His Met Asp Ile
100 105 110

Phe Gln Asn Leu Ala Val Asp Leu Asp Thr Glu Gly Arg Tyr Leu Phe
115 120 125

Leu Asn Ala Ile Ala Asn Gln Leu Arg Tyr Pro Asn Ser His Thr His
130 135 140

Tyr Phe Ser Cys Thr Met Leu Tyr Leu Phe Ala Glu Ala Asn Thr Glu
145 150 155 160

Ala Ile Gln Glu Gln Ile Thr Arg Val Leu Leu Glu Arg Leu Ile Val
165 170 175

Asn Arg Pro His Pro Trp Gly Leu Leu Ile Thr Phe Ile Glu Leu Ile
180 185 190

Lys Asn Pro Ala Phe Lys Phe Trp Asn His Glu Phe Val His Cys Ala
195 200 205

Pro Glu Ile Glu Lys Leu Phe Gln Ser Val Ala Gln Cys Cys Met Gly
210 215 220

Gln Lys Gln Ala Gln Gln Val Met Glu Gly Thr Gly Ala Ser

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225

230

235

<210> 2

<211> 339

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu

1

5

10

15

Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn

20

25

30

Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His

35

40

45

Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu

50

55

60

Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val

65

70

75

80

Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu

85

90

95

Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val

100

105

110

Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly

115

120

125

Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln

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| | | | |
|---|-----|-----|-----|
| 130 | 135 | 140 | |
| Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp | | | |
| 145 | 150 | 155 | 160 |
| Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu | | | |
| | 165 | 170 | 175 |
| Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu | | | |
| | 180 | 185 | 190 |
| Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro | | | |
| | 195 | 200 | 205 |
| Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro | | | |
| 210 | 215 | 220 | |
| Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His | | | |
| 225 | 230 | 235 | 240 |
| Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr | | | |
| | 245 | 250 | 255 |
| Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile | | | |
| | 260 | 265 | 270 |
| Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp | | | |
| | 275 | 280 | 285 |
| Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn | | | |
| 290 | 295 | 300 | |
| Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys | | | |
| 305 | 310 | 315 | 320 |
| Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr | | | |
| | 325 | 330 | 335 |

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Arg Arg Arg

<210> 3

<211> 326

<212> PRT

<213> Homo sapiens

<400> 3

Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln Arg Thr Leu

1 5 10 15

Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser Thr Thr Ser

20 25 30

Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val Pro Lys Pro

35 40 45

Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp Met Pro Val Ser

50 55 60

Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val Val Gln Tyr Asn

65 70 75 80

Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe Arg Ser Phe Arg Ser Gly

85 90 95

Met Trp Leu Ser Cys Glu Glu Thr Val Glu Glu Pro Gly Glu Arg Cys

100 105 110

Arg Ser Phe Ile Glu Leu Thr Pro Pro Ala Lys Arg Glu Ile Leu Trp

115 120 125

Leu Ser Leu Gly Thr Gln Ile Thr Tyr Ile Gly Leu Gln Phe Ile Ser

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130 135 140
Phe Leu Leu Leu Leu Thr Asp Leu Leu Leu Thr Gly Asn Pro Ala Cys
145 150 155 160
Gly Leu Lys Leu Ser Ala Phe Ala Ala Val Ser Ser Val Leu Ser Gly
165 170 175
Leu Leu Gly Met Val Ala His Met Met Tyr Ser Gln Val Phe Gln Ala
180 185 190
Thr Val Asn Leu Gly Pro Glu Asp Trp Arg Pro His Val Trp Asn Tyr
195 200 205
Gly Trp Ala Phe Tyr Met Ala Trp Leu Ser Phe Thr Cys Cys Met Ala
210 215 220
Ser Ala Val Thr Thr Phe Asn Thr Tyr Thr Arg Met Val Leu Glu Phe
225 230 235 240
Lys Cys Lys His Ser Lys Ser Phe Lys Glu Asn Pro Asn Cys Leu Pro
245 250 255
His His His Gln Cys Phe Pro Arg Arg Leu Ser Ser Ala Ala Pro Thr
260 265 270
Val Gly Pro Leu Thr Ser Tyr His Gln Tyr His Asn Gln Pro Ile His
275 280 285
Ser Val Ser Glu Gly Val Asp Phe Tyr Ser Glu Leu Arg Asn Lys Gly
290 295 300
Phe Gln Arg Gly Ala Ser Gln Glu Leu Lys Glu Ala Val Arg Ser Ser
305 310 315 320
Val Glu Glu Glu Gln Cys

325

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<210> 4

<211> 324

<212> PRT

<213> Homo sapiens

<400> 4

Met Ala Ala Ala Ala Pro Gly Asn Gly Arg Ala Ser Ala Pro Arg Leu

1 5 10 15

Leu Leu Leu Phe Leu Val Pro Leu Leu Trp Ala Pro Ala Ala Val Arg

20 25 30

Ala Gly Pro Asp Glu Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala

35 40 45

Pro Ala Gln Gln Leu Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu

50 55 60

Pro Ala Arg Val Glu Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr

65 70 75 80

Asn Lys Glu Asp Pro Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala

85 90 95

Phe Val Ala Ala Ile Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys

100 105 110

Thr Phe Phe Ile Ala Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr

115 120 125

Val Leu Ala Gly Ala Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser

130 135 140

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Val Leu Phe Gly Tyr Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr
145 150 155 160
Tyr Val Ser Thr Val Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg
165 170 175
Glu Gly Leu Lys Met Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu
180 185 190
Val Gln Ala Glu Leu Lys Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys
195 200 205
Leu Leu Asn Gly Pro Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val
210 215 220
Pro Gln Lys Lys Trp Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala
225 230 235 240
Leu Thr Leu Thr Phe Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr
245 250 255
Thr Ile Val Leu Ala Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly
260 265 270
Gly Thr Val Gly His Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly
275 280 285
Arg Met Ile Ala Gln Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly
290 295 300
Gly Ile Val Phe Leu Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro
305 310 315 320
Asp Ser Gly Phe

<210> 5

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<211> 153

<212> PRT

<213> Homo sapiens

<400> 5

Met Asn Val Gly Thr Ala His Ser Glu Val Asn Pro Asn Thr Arg Val

1 5 10 15

Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu

20 25 30

Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val

35 40 45

Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu

50 55 60

His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala

65 70 75 80

Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr

85 90 95

Ala Ser Arg Lys Phe Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu

100 105 110

Thr Ser Phe Tyr Thr Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr

115 120 125

Val Ser Leu Met Ser Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly

130 135 140

Val Arg Ile Phe Gly Ile Asn Lys Tyr

145 150

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<210> 6

<211> 153

<212> PRT

<213> Homo sapiens

<400> 6

Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg Val

1 5 10 15

Met Asn Ser Arg Gly Ile Trp Leu Ala Tyr Ile Ile Leu Val Gly Leu

20 25 30

Leu His Met Val Leu Leu Ser Ile Pro Phe Phe Ser Ile Pro Val Val

35 40 45

Trp Thr Leu Thr Asn Val Ile His Asn Leu Ala Thr Tyr Val Phe Leu

50 55 60

His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala

65 70 75 80

Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Leu Gln Phe Thr

85 90 95

Ser Ser Arg Lys Phe Leu Ser Ile Ser Pro Ile Val Leu Tyr Leu Leu

100 105 110

Ala Ser Phe Tyr Thr Lys Tyr Asp Ala Ala His Phe Leu Ile Asn Thr

115 120 125

Ala Ser Leu Leu Ser Val Leu Leu Pro Lys Leu Pro Gln Phe His Gly

130 135 140

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Val Arg Val Phe Gly Ile Asn Lys Tyr

145

150

<210> 7

<211> 200

<212> PRT

<213> Homo sapiens

<400> 7

Met Ala Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala

1

5

10

15

Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp

20

25

30

Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe

35

40

45

Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg

50

55

60

Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu

65

70

75

80

Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val

85

90

95

Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe

100

105

110

Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser

115

120

125

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Leu Ala Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val

130

135

140

Pro Leu Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr Leu Cys

145

150

155

160

Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met

165

170

175

Phe Gly Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr

180

185

190

Leu Glu Lys Thr Ile His Glu Glu

195

200

<210> 8

<211> 189

<212> PRT

<213> Homo sapiens

<400> 8

Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Gly Ala Trp Ala

1

5

10

15

Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro

20

25

30

Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu

35

40

45

Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu

50

55

60

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Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg

65 70 75 80

Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Ser Cys Ser

85 90 95

Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg

100 105 110

Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val

115 120 125

Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu

130 135 140

His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln

145 150 155 160

Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly

165 170 175

Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu

180 185

<210> 9

<211> 714

<212> DNA

<213> Homo sapiens

<400> 9

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aacattgctc cccggattct caccaatttc actggagtaa tgccacctca gttcaaaaag 120

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gatttggatt cctatcttaa aactcgatca ccagtcactt tcctgtctga tctgcgcagc 180
aacctacagg tatccaatga acctgggaat cgctacaacc tccagctcat caatgcactg 240
gtgctctatg tcgggactca ggccattgcg cacatccaca acaagggcag cacaccttca 300
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agccacactc actacttcag ttgcaccatg ctgtacctt ttgcagaggc caatacggaa 480
gccatccaag aacagatcac aagagttctc ttggaacggt tgattgtaa taggccacat 540
ccttggggtc ttcttattac cttcattgag ctgattaaaa acccagcgtt taagttcttg 600
aaccatgaat ttgtacactg tgccccagaa atcgaaaagt tattccagtc ggtcgcacag 660
tgctgcatgg gacagaagca ggcccagcaa gtaatggaag ggacaggtgc cagt 714

<210> 10

<211> 1017

<212> DNA

<213> Homo sapiens

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gatgtaaaag ctcttaccct ccactatgac cgctatacca cctcccgcag gctggatccc 180
atcccacagt tgaaatgtgt tggaggcaca gctggttgtg attcttatac cccaaaagtc 240
atacagtgtc agaacaaagg ctgggatggg tatgatgtac agtgggaatg taagacggac 300
ttagatattg catacaaatt tggaaaaact gtggtgagct gtgaaggcta tgagtcctct 360
gaagaccagt atgtactaag aggttcttgt ggcttggagt ataatttaga ttatacagaa 420
cttggcctgc agaaaactgaa ggagtctgga aagcagcacg gctttgcctc tttctctgat 480

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tattattata agtggctctc ggccgattcc tgtaacatga gtggattgat taccatcgtg 540
gtactccttg ggatcgctt tgtagtctat aagctgttcc tgagtgcagg gcagtattct 600
cctccaccgt actctgagta tccctcattt tcccaccgtt accagagatt caccaactca 660
gcaggacctc ctccccagg ctttaagtct gagttcacag gaccacagaa tactggccat 720
ggtgcaactt ctggttttgg cagtgccttt acaggacaac aaggatatga aaattcagga 780
ccagggttct ggacaggctt gggaactggg ggaatactag gatatttgtt tggcagcaat 840
agagcggcaa cacccttctc agactcgtgg tactaccgt cctatcctcc ctccctaccct 900
ggcacgtgga atagggctta ctacccctt catggaggct cgggcagcta ttcggtatgt 960
tcaaactcag acacgaaaac cagaactgca tcaggatatg gtggtaccag gagacga 1017

<210> 11

<211> 978

<212> DNA

<213> Homo sapiens

<400> 11

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ggcacacaga aggtgccccaa gccctgtgac gagaaaggac tggcagccaa gtgctttgac 180
atgccagtgt ccttggtatg agataccaac acatccacc aggaggtggg acaatacaac 240
tgaggagactg gggatgaccg gttctccttc cggagcttcc ggagtggcat gtggctatcc 300
tgtgaggaaa ctgtggaaga accaggggag aggtgccgaa gtttcattga acttacacca 360
ccagccaaga gagaaatcct atggttatcc ctgggaacgc agatcaccta catcggaatt 420
caattcatca gttcctcct gctactaaca gacttgctac tcaactgggaa ccctgcctgt 480
gggtcctaac tgagcgctt tgctgctgtt tccctgttcc tgtcaggctt cctggggatg 540

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gtggcccaca tgatgtattc acaagtcttc caagcgactg tcaacttggg tccagaagac 600
 tggagaccac atgtttggaa ttatggctgg gccttctaca tggcctggct ctcttcacc 660
 tgctgcatgg cgtcggctgt caccaccttc aacacgtaca ccaggatggt gctggagttc 720
 aagtgcagc atagtaagag cttcaaggaa aaccggaact gctaccaca tcaccatcag 780
 tgtttccctc ggcggtgtc aagtgcagcc cccaccgtgg gtctttgac cagctaccac 840
 cagtatcata atcagcccat ccactctgtc tctgaggag tgcacttcta ctccgagctg 900
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 gtagaggaag agcagtgt 978

<210> 12

<211> 972

<212> DNA

<213> Homo sapiens

<400> 12

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 caccggaaca aagaaccgcc ggcgccggcc cagcagctgc agccgcagcc tgtggctgtg 180
 cagggccccg agccggcccc ggtcgagaaa atatttacac cagcagctcc agttcatacc 240
 aataaagaag atcctgtac ccaaactaat ttgggattta tccatgcatt tgctgctgcc 300
 atatcagtta ttattgtatc tgaattgggt gataagacat tttttatagc agccatcatg 360
 gcaatgcgt ataaccgct gaccgtgctg gctggtgcaa tgcttgctt gggactaatg 420
 acatgctgt cagttttgtt tggctatgcc accacagtca tccccagggt ctatacatc 480
 tatgtttcaa ctgtattatt tgccattttt ggcattagaa tgcttcggga aggcttaaag 540
 atgagccctg atgagggtca agaggaactg gaagaagttc aagctgaatt aaagaagaaa 600

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gatgaagaat ttcaacgaac caaactttta aatggaccgg gagatgttga aacgggtaca 660
 agcataacag tacctcagaa aaagtgggtg ctttttattt cacccatttt tgttcaagct 720
 cttacattaa cattcttagc agaatggggt gatcgctctc aactaactac aattgtattg 780
 gcagctagag aggacccta tgggtgtagcc gtgggtggaa ctgtggggca ctgcctgtgc 840
 acgggattgg cagtaattgg aggaagaatg atagcacaga aaatctctgt cagaactgtg 900
 acaatcatag gaggcacgtg ttttttggcg tttgcatttt ctgcactatt tataagccct 960
 gattctggtt tt 972

<210> 13

<211> 459

<212> DNA

<213> Homo sapiens

<400> 13

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 ccgtttgtga gtgtccctgt cgtctggacc ctcaccaacc tcattcacia catgggcatg 180
 tatatcticc tgcacacggt gaaggggaca ccctttgaga ccccggaaca gggcaaggcg 240
 aggctgctaa cccactggga gcagatggat tatgggggtc agttcacggc ctctcggaag 300
 ttcttgacca tcacacccat cgtgctgtac ttcctacca gcttctacac taagtacgac 360
 cagatccatt ttgtgtcaa caccgtgtcc ctgatgagcg tgcttatccc caagctgccc 420
 cagctccacg gagtccgat ttttggaatc aataagtac 459

<210> 14

<211> 459

18/41

<212> DNA

<213> Homo sapiens

<400> 14

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atgaatgtgg ggggtggcaca cagcgaagta aacccaaca cccgagtgat gaatagccga      60
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cccttcttca gcattcctgt tgtctggacc ctgaccaacg tcatccataa cctggctacg      180
tatgtcttcc ttcatacggg gaaagggaca cccttgaga ctctgacca aggaaaggct      240
cggctactga cacactggga gcaaattggac tatgggctcc agtttacctc tccccgaag      300
ttcctcagca tctctcctat tgtgctctat ctctggcca gttctatac caagtatgat      360
gctgcgcact tctcatcaa cacagcctca ttgctaagtg tactgctgcc gaagttgccc      420
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<210> 15

<211> 600

<212> DNA

<213> Homo sapiens

<400> 15

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aatatatatc aaatggcgac atttggaaac acagctgggt tctctggaat attctcaaac      180
ttcctgttca gacgctgctt caaggttaaa catgatgctt tgaagacata tgcattcattg      240
gctacacttc catttttgtc tactgtttgt actgacaagc tttttgtaat tgatgctttg      300
tattcagata atataagcaa ggaaaactgt gttttcagaa gctcactgat tggcatagtt      360
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tgtggtgttt tctatcccag ttctttggct ttactaaaa atggacgcct ggcaaccaag 420
tatcataccg ttccactgcc accaaaagga agggttttta tccattggat gacgctttgt 480
caaacacaaa tgaaattaat ggcgattcct ctagtctttc agattatgtt tggaatatta 540
aatggtctat accattatgc agtatttgaa gagacacttg agaaaactat acatgaagag 600

<210> 16

<211> 567

<212> DNA

<213> Homo sapiens

<400> 16

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ctcggggaca gggcgccact cacagccaca gccccacaac tggatgatga ggagatgtac 120
tcagcccaca tgcccgtca cctgcgctgt gatgcctgca gagctgtggc ttaccagatg 180
tggcaaaatc tggcaaaggc agagaccaa cttcatacct caaactctgg gggcgggcgg 240
gagctgagcg agttggtcta cacggatgtc ctggaccgga gctgctcccg gaactggcag 300
gactacggag ttcgagaagt ggaccaagt aaacgtctca caggcccagg acttagcgag 360
gggccagagc caagcatcag cgtgatggc acagggggcc cctggcctac caggctctcc 420
aggacatgtt tgcactactt gggggagttt ggagaagacc agatctatga agcccaccaa 480
caaggccgag gggctctgga ggcattgcta tgtggggggac cccagggggc ctgctcagag 540
aaggtgtcag ccacaagaga agagctc 567

<210> 17

<211> 1167

<212> DNA

20/41

<213> Homo sapiens

<220>

<221> CDS

<222> (187)... (903)

<400> 17

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 tatagtgtat atagtttttag aaaaacagtc ccaccactta agcatagatg taatttacta 180
 ataaaa atg att ctg ctt gtg att ctt gca ttt tat ctg tgg cag gtg 228

Met Ile Leu Leu Val Ile Leu Ala Phe Tyr Leu Trp Gln Val

1

5

10

gac atg ttg agt gaa att aac att gct ccc cgg att ctc acc aat ttc 276

Asp Met Leu Ser Glu Ile Asn Ile Ala Pro Arg Ile Leu Thr Asn Phe

15

20

25

30

act gga gta atg cca cct cag ttc aaa aag gat ttg gat tcc tat ctt 324

Thr Gly Val Met Pro Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu

35

40

45

aaa act cga tca cca gtc act ttc ctg tct gat ctg cgc agc aac cta 372

Lys Thr Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu

50

55

60

cag gta tcc aat gaa cct ggg aat cgc tac aac ctc cag ctc atc aat 420

Gln Val Ser Asn Glu Pro Gly Asn Arg Tyr Asn Leu Gln Leu Ile Asn

65

70

75

21/41

| | |
|---|-----|
| gca ctg gtg ctc tat gtc ggg act cag gcc att gcg cac atc cac aac | 468 |
| Ala Leu Val Leu Tyr Val Gly Thr Gln Ala Ile Ala His Ile His Asn | |
| 80 85 90 | |
| aag ggc agc aca cct tca atg agc acc atc act cac tca gca cac atg | 516 |
| Lys Gly Ser Thr Pro Ser Met Ser Thr Ile Thr His Ser Ala His Met | |
| 95 100 105 110 | |
| gat atc ttc cag aat ttg gct gtg gac ttg gac act gag ggt cgc tat | 564 |
| Asp Ile Phe Gln Asn Leu Ala Val Asp Leu Asp Thr Glu Gly Arg Tyr | |
| 115 120 125 | |
| ctc ttt ttg aat gca att gca aat cag ctc cgg tac cca aat agc cac | 612 |
| Leu Phe Leu Asn Ala Ile Ala Asn Gln Leu Arg Tyr Pro Asn Ser His | |
| 130 135 140 | |
| act cac tac ttc agt tgc acc atg ctg tac ctt ttt gca gag gcc aat | 660 |
| Thr His Tyr Phe Ser Cys Thr Met Leu Tyr Leu Phe Ala Glu Ala Asn | |
| 145 150 155 | |
| acg gaa gcc atc caa gaa cag atc aca aga gtt ctc ttg gaa cgg ttg | 708 |
| Thr Glu Ala Ile Gln Glu Gln Ile Thr Arg Val Leu Leu Glu Arg Leu | |
| 160 165 170 | |
| att gta aat agg cca cat cct tgg ggt ctt ctt att acc ttc att gag | 756 |
| Ile Val Asn Arg Pro His Pro Trp Gly Leu Leu Ile Thr Phe Ile Glu | |
| 175 180 185 190 | |
| ctg att aaa aac cca gcg ttt aag ttc tgg aac cat gaa ttt gta cac | 804 |
| Leu Ile Lys Asn Pro Ala Phe Lys Phe Trp Asn His Glu Phe Val His | |
| 195 200 205 | |
| tgt gcc cca gaa atc gaa aag tta ttc cag tcg gtc gca cag tgc tgc | 852 |

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Cys Ala Pro Glu Ile Glu Lys Leu Phe Gln Ser Val Ala Gln Cys Cys

210

215

220

atg gga cag aag cag gcc cag caa gta atg gaa ggg aca ggt gcc agt 900

Met Gly Gln Lys Gln Ala Gln Gln Val Met Glu Gly Thr Gly Ala Ser

225

230

235

tagacgaaac tgcatctctg ttgtacgtgt cagtctagag gtctcactgc accgagttca 960

taaactgact gaagaatcct ttcagctctt cctgactttc ccagcccttt ggtttgtggg 1020

tatctgcccc aactactgtt gggatcagcc tctgtctta tgtgggcacg ttccaaagtt 1080

taaatgcatt tttttgactc ttggccaaaa tttagaagat gctgtgaata tcattttgaa 1140

cttgtgtaaa tacatgaaag agaaaac 1167

<210> 18

<211> 1925

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (115)... (1134)

<400> 18

gttccttcgc cgccgccagg ggtagcgggtg tagctgcgca gcgtcgcgcg cgtaccgca 60

cccaggttcg gcccgtaggc gtctggcage ccggcgccat cttcatcgag cgcc atg 117

Met

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gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc 165
 Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly
 5 10 15
 ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac 213
 Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp
 20 25 30
 cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat 261
 Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr
 35 40 45
 gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa 309
 Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys
 50 55 60 65
 tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata 357
 Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile
 70 75 80
 cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt 405
 Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys
 85 90 95
 aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc 453
 Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser
 100 105 110
 tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct 501
 Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser
 115 120 125
 tgt ggc ttg gag tat aat tta gat tat aca gaa ctt ggc ctg cag aaa 549

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Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys
 130 135 140 145
 ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat 597
 Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr
 150 155 160
 tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att 645
 Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile
 165 170 175
 acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc 693
 Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe
 180 185 190
 ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca 741
 Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro
 195 200 205
 ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc 789
 Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro
 210 215 220 225
 cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggc cat ggt 837
 Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly
 230 235 240
 gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa 885
 Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu
 245 250 255
 aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta 933
 Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu

25/41

| | | | |
|--|-----|-----|------|
| 260 | 265 | 270 | |
| gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg | | | 981 |
| Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser | | | |
| 275 | 280 | 285 | |
| tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg | | | 1029 |
| Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg | | | |
| 290 | 295 | 300 | 305 |
| gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca | | | 1077 |
| Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser | | | |
| 310 | 315 | 320 | |
| aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg | | | 1125 |
| Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg | | | |
| 325 | 330 | 335 | |
| aga cga taaagtagaa agttggagtc aaacactgga tgcagaaatt ttggatttt | | | 1180 |
| Arg Arg | | | |
| | | | |
| tcataccttt ctcttttagaa aaaaagtact acctgttaac aattgggaaa aggggatatt | | | 1240 |
| caaaagtctt gtggtgttat gtccagtgt gctttttgta ttctattatt tgaggctaaa | | | 1300 |
| agttgatgtg tgacaaaata cttatgtgtt gtatgtcagt gtaacatgca gatgtatatt | | | 1360 |
| gcagtttttg aaagtgatca ttactgtgga atgctaaaaa tacattaatt tctaaaacct | | | 1420 |
| gtgatgccct aagaagcatt aagaatgaag gtgttgtact aatagaaact aagtacagaa | | | 1480 |
| aatttcagtt ttaggtgggt gtagctgatg agttattacc tcatagagac tataatatcc | | | 1540 |
| tatttggtat tatattattt gatgtttgct gttcttcaaa catttaaatac aagctttgga | | | 1600 |
| ctaattatgc taatttgtga gttctgatca cttttgagct ctgaagcttt gaatcattca | | | 1660 |
| gtggtggaga tggccttctg gtaactgaat attaccttct gtaggaaaag gtggaaaata | | | 1720 |

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agcatctaga aggttgttgt gaatgactct gtgctggcaa aaatgcttga aacctctata 1780
 ttcttttctg tcataagagg taaagggtcaa atttttcaac aaaagtcttt taataacaaa 1840
 agcatgcagt tctctgtgaa atctcaaata ttgttgtaat agtctgtttc aatcttaaaa 1900
 agaatacaata aaaacaaaca agggg 1925

<210> 19

<211> 1125

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (71)... (1051)

<400> 19

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gacgctgacc atg gcc aag atg gag ctc tcg aag gcc ttc tct ggc cag 109

Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln

1

5

10

cgg aca ctc cta tct gcc atc ctc agc atg cta tca ctc agc ttc tcc 157

Arg Thr Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser

15

20

25

aca aca tcc ctg ctc agc aac tac tgg ttt gtg ggc aca cag aag gtg 205

Thr Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val

30

35

40

45

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| | |
|---|-----|
| ccc aag ccc ctg tgc gag aaa ggt ctg gca gcc aag tgc ttt gac atg | 253 |
| Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp Met | |
| 50 55 60 | |
| cca gtg tcc ctg gat gga gat acc aac aca tcc acc cag gag gtg gta | 301 |
| Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val Val | |
| 65 70 75 | |
| caa tac aac tgg gag act ggg gat gac cgg ttc tcc ttc cgg agc ttc | 349 |
| Gln Tyr Asn Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe Arg Ser Phe | |
| 80 85 90 | |
| cgg agt ggc atg tgg cta tcc tgt gag gaa act gtg gaa gaa cca ggg | 397 |
| Arg Ser Gly Met Trp Leu Ser Cys Glu Glu Thr Val Glu Glu Pro Gly | |
| 95 100 105 | |
| gag agg tgc cga agt ttc att gaa ctt aca cca cca gcc aag aga gaa | 445 |
| Glu Arg Cys Arg Ser Phe Ile Glu Leu Thr Pro Pro Ala Lys Arg Glu | |
| 110 115 120 125 | |
| atc cta fgg tta tcc ctg gga acg cag atc acc tac atc gga ctt caa | 493 |
| Ile Leu Trp Leu Ser Leu Gly Thr Gln Ile Thr Tyr Ile Gly Leu Gln | |
| 130 135 140 | |
| ttc atc agc ttc ctc ctg cta cta aca gac ttg cta ctc act ggg aac | 541 |
| Phe Ile Ser Phe Leu Leu Leu Leu Thr Asp Leu Leu Leu Thr Gly Asn | |
| 145 150 155 | |
| cct gcc tgt ggg ctc aaa ctg agc gcc ttt gct gct gtt tcc tct gtc | 589 |
| Pro Ala Cys Gly Leu Lys Leu Ser Ala Phe Ala Ala Val Ser Ser Val | |
| 160 165 170 | |
| ctg tca ggt ctc ctg ggg atg gtg gcc cac atg atg tat tca caa gtc | 637 |

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Leu Ser Gly Leu Leu Gly Met Val Ala His Met Met Tyr Ser Gln Val
 175 180 185
 ttc caa gcg act gtc aac ttg ggt cca gaa gac tgg aga cca cat gtt 685
 Phe Gln Ala Thr Val Asn Leu Gly Pro Glu Asp Trp Arg Pro His Val
 190 195 200 205
 tgg aat tat ggc tgg gcc ttc tac atg gcc tgg ctc tcc ttc acc tgc 733
 Trp Asn Tyr Gly Trp Ala Phe Tyr Met Ala Trp Leu Ser Phe Thr Cys
 210 215 220
 tgc atg gcg tcg gct gtc acc acc ttc aac acg tac acc agg atg gtg 781
 Cys Met Ala Ser Ala Val Thr Thr Phe Asn Thr Tyr Thr Arg Met Val
 225 230 235
 ctg gag ttc aag tgc aag cat agt aag agc ttc aag gaa aac ccg aac 829
 Leu Glu Phe Lys Cys Lys His Ser Lys Ser Phe Lys Glu Asn Pro Asn
 240 245 250
 tgc cta cca cat cac cat cag tgt ttc cct cgg cgg ctg tca agt gca 877
 Cys Leu Pro His His His Gln Cys Phe Pro Arg Arg Leu Ser Ser Ala
 255 260 265
 gcc ccc acc gtg ggt cct ttg acc agc tac cac cag tat cat aat cag 925
 Ala Pro Thr Val Gly Pro Leu Thr Ser Tyr His Gln Tyr His Asn Gln
 270 275 280 285
 ccc atc cac tct gtc tct gag gga gtc gac ttc tac tcc gag ctg cgg 973
 Pro Ile His Ser Val Ser Glu Gly Val Asp Phe Tyr Ser Glu Leu Arg
 290 295 300
 aac aag gga ttt caa aga ggg gcc agc cag gag ctg aaa gaa gca gtt 1021
 Asn Lys Gly Phe Gln Arg Gly Ala Ser Gln Glu Leu Lys Glu Ala Val

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305 310 315
 agg tca tct gta gag gaa gag cag tgt taggagttaa gcgggtttgg gg 1070
 Arg Ser Ser Val Glu Glu Glu Gln Cys

320 325
 agtaggcttg agccctacct tacacgtctg ctgattatca acatgtgctt aagcc 1125

<210> 20

<211> 1734

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (40)... (1014)

<400> 20

ctcttgcggc gcccgtagcg gcccgggcccg gcaggcggg atg gcg gcc gcg gct 54

Met Ala Ala Ala Ala

1 5

ccg ggg aac ggc cgc gca tcg gcg ccc cgg ctg ctt ctg ctc ttt ctg 102

Pro Gly Asn Gly Arg Ala Ser Ala Pro Arg Leu Leu Leu Leu Phe Leu

10 15 20

gtt ccg ctg ctg tgg gcc ccg gct gcg gtc cgg gcc ggc cca gat gaa 150

Val Pro Leu Leu Trp Ala Pro Ala Ala Val Arg Ala Gly Pro Asp Glu

25 30 35

30/41

| | |
|---|-----|
| gac ctt agc cac cgg aac aaa gaa ccg ccg gcg ccg gcc cag cag ctg | 198 |
| Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala Pro Ala Gln Gln Leu | |
| 40 45 50 | |
| cag ccg cag cct gtg gct gtg cag ggc ccc gag ccg gcc cgg gtc gag | 246 |
| Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu Pro Ala Arg Val Glu | |
| 55 60 65 | |
| aaa ata ttt aca cca gca gct cca gtt cat acc aat aaa gaa gat cct | 294 |
| Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr Asn Lys Glu Asp Pro | |
| 70 75 80 85 | |
| gct acc caa act aat ttg gga ttt atc cat gca ttt gtc gct gcc ata | 342 |
| Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala Phe Val Ala Ala Ile | |
| 90 95 100 | |
| tca gtt att att gta tct gaa ttg ggt gat aag aca ttt ttt ata gca | 390 |
| Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys Thr Phe Phe Ile Ala | |
| 105 110 115 | |
| gcc atc atg gca atg cgc tat aac cgc ctg acc gtg ctg gct ggt gca | 438 |
| Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala | |
| 120 125 130 | |
| atg ctt gcc ttg gga cta atg aca tgc ttg tca gtt ttg ttt ggc tat | 486 |
| Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr | |
| 135 140 145 | |
| gcc acc aca gtc atc ccc agg gtc tat aca tac tat gtt tca act gta | 534 |
| Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr Tyr Val Ser Thr Val | |
| 150 155 160 165 | |
| tta ttt gcc att ttt ggc att aga atg ctt cgg gaa ggc tta aag atg | 582 |

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Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg Glu Gly Leu Lys Met
 170 175 180
 agc cct gat gag ggt caa gag gaa ctg gaa gaa gtt caa gct gaa tta 630
 Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu Val Gln Ala Glu Leu
 185 190 195
 aag aag aaa gat gaa gaa ttt caa cga acc aaa ctt tta aat gga ccg 678
 Lys Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys Leu Leu Asn Gly Pro
 200 205 210
 gga gat gtt gaa acg ggt aca agc ata aca gta cct cag aaa aag tgg 726
 Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val Pro Gln Lys Lys Trp
 215 220 225
 ttg cat ttt att tca ccc att ttt gtt caa gct ctt aca tta aca ttc 774
 Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala Leu Thr Leu Thr Phe
 230 235 240 245
 tta gca gaa tgg ggt gat cgc tct caa cta act aca att gta ttg gca 822
 Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr Thr Ile Val Leu Ala
 250 255 260
 gct aga gag gac ccc tat ggt gta gcc gtg ggt gga act gtg ggg cac 870
 Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly Gly Thr Val Gly His
 265 270 275
 tgc ctg tgc acg gga ttg gca gta att gga gga aga atg ata gca cag 918
 Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly Arg Met Ile Ala Gln
 280 285 290
 aaa atc tct gtc aga act gtg aca atc ata gga ggc atc gtt ttt ttg 966
 Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly Gly Ile Val Phe Leu

32/41

| 295 | 300 | 305 | |
|--|-----|-----|------|
| gcg ttt gca ttt tct gca cta ttt ata agc cct gat tct ggt ttt | | | 1011 |
| Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro Asp Ser Gly Phe | | | |
| 310 | 315 | 320 | |
| taacgctgt ttgttcatt atatttagtt taaaataggt agtattatct ttctgtacat | | | 1070 |
| agtgtacatt acaactaaaa gtgatggaaa aatactgtat ttgttagcac tgattttgtg | | | 1130 |
| agtttgaccc attattatgt ctgagatata atcattgatt ctatttgtaa caaggagttt | | | 1190 |
| taaaagaaac ctgacttcta agtgtgggtt tttcttctct ccaacataat tatgttaata | | | 1250 |
| tggctcctcat ttttcttttg gtgcagaacc gttgtgcagt ggggtctacc atgcaatttt | | | 1310 |
| ctttcagcac tgaccctttt ttaaggaata caaattttct ctttcattcac ttaggtgttt | | | 1370 |
| taagatgttt accttaaagt ttttcttggg gaaagaatga attaatttct atttcttaaa | | | 1430 |
| acatttcctt gagccagtaa acagtagttt aatcattggt cttttcaaaa ctaggtgttt | | | 1490 |
| aaaaaaagag acatatatga tattgtgttt atatcaataa catggcacia caagaactgt | | | 1550 |
| ctgccaggtc attcttcttc tttttttttt aattgggtag gacaccaat ataaaaacag | | | 1610 |
| tcaatatttg acaatgtgga attaccaa ataaaagagaa tactatgaat gtattcatat | | | 1670 |
| tttttctata ttgaataaac aatgtaacat agataacaat ataaataaaa gtggtatgac | | | 1730 |
| cagt | | | 1734 |

<210> 21

<211> 2064

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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<222> (98)... (559)

<400> 21

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| aaaacagctg ctggagcagc agcggccccc gctcccggga accgttcccg ggccgttgat | 60 |
| cttcggcccc acacgaacag cagagagggg cagcagg atg aat gtg ggc aca | 112 |
| Met Asn Val Gly Thr | |
| 1 5 | |
| gcg cac agc gag gtg aac ccc aac acg cgg gtg atg aac agc cgt ggc | 160 |
| Ala His Ser Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly | |
| 10 15 20 | |
| atc tgg ctc tcc tac gtg ctg gcc atc ggt ctc ctc cac atc gtg ctg | 208 |
| Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu Leu His Ile Val Leu | |
| 25 30 35 | |
| ctg agc atc ccg ttt gtg agt gtc cct gtc gtc tgg acc ctc acc aac | 256 |
| Leu Ser Ile Pro Phe Val Ser Val Pro Val Val Trp Thr Leu Thr Asn | |
| 40 45 50 | |
| ctc att cac aac atg ggc atg tat atc ttc ctg cac acg gtg aag ggg | 304 |
| Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu His Thr Val Lys Gly | |
| 55 60 65 | |
| aca ccc ttt gag acc ccg gac cag ggc aag gcg agg ctg cta acc cac | 352 |
| Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His | |
| 70 75 80 85 | |
| tgg gag cag atg gat tat ggg gtc cag ttc acg gcc tct cgg aag ttc | 400 |
| Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr Ala Ser Arg Lys Phe | |
| 90 95 100 | |

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ttg acc atc aca ccc atc gtg ctg tac ttc ctc acc agc ttc tac act 448
 Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu Thr Ser Phe Tyr Thr
 105 110 115
 aag tac gac cag atc cat ttt gtg ctc aac acc gtg tcc ctg atg agc 496
 Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr Val Ser Leu Met Ser
 120 125 130
 gtg ctt atc ccc aag ctg ccc cag ctc cac gga gtc cgg att ttt gga 544
 Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly Val Arg Ile Phe Gly
 135 140 145
 atc aat aag tac tgagagtga gcccttccc ctgccaggg tggcagggga gggg 600
 Ile Asn Lys Tyr
 150
 tagggtaaaa ggcattgtgt gcaacactga agacagaaag aagaagcctc tggacactgc 660
 cagagatggg ggttgagcct ctggcctaata tccccccctc gcttccccca gtagccaact 720
 tggagtagct ttagtggtggg ttggggtagg ccccttgggc tctgaccttt tctgaatttt 780
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 gctcacttgt ttgccctcag gcagccaaag cactttaacc cctgcatagg gagcagaggg 960
 cggtacggct tctggattgt ttcaactgtga ttcttaggtt ttttcgatgc cacgcagtgt 1020
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 tctaatacaa gtcccaggct tttggcagct tctctgcaac ccaccgtggg tcttggttgg 1140
 gagtggggag ggtcagggtg gggaaagatg gggtagagtg tagatggctt ggttccagag 1200
 gtgagggggc cagggctgct gccatcctgg cctgggtggag gttggggagc tgtaggagag 1260
 ctagtgagtc gagacttaga agaattggggc cacatagcag cagaggactg gtgtaaggga 1320
 gggaggggta gggacagaag ctagacccaa tctcctttgg gatgtgggca gggaggggaag 1380

35/41

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caggcttggg gggtaattt acccacagaa tgtgatagta ataggggagg gaggctgctg 1440
tgggtttaac tcctgggttg gctgttgggt agacaggtgg ggaaaaggcc cgtgagtcac 1500
tgtaagcaca ggtccaactt ggccctgact cctgcggggg tatggggaag ctgtgacaga 1560
aacgatgggt gctgtgttcc tctgcaggcc ctcacccctt aacttcctca tacagactgg 1620
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gggctggagc cttctcccct cccagtttg actaggggca gtgttaattt tgaaaagggtg 1860
tgggtccctg tgcctcttc caggggtcca agggaacagg agaggtcact gggcctgttt 1920
tctccctcct gaccctgcat ctcccacccc gtgtatcata gggaactttc accttaaaat 1980
ctttctaagc aaagtgtgaa taggattttt actccctttg tacagtattc tgagaaacgc 2040
aaataaaagg gcaacatgtt tctg 2064

```

<210> 22

<211> 570

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (28)... (489)

<400> 22

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agccggacgg ggatctgagc tggcagg atg aat gtg ggg gtg gca cac agc 51

```

Met Asn Val Gly Val Ala His Ser

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| | | |
|---|-----|-----|
| 1 | 5 | |
| gaa gta aac ccc aac acc cga gtg atg aat agc cga ggc atc tgg ctg | | 99 |
| Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly Ile Trp Leu | | |
| 10 | 15 | 20 |
| gcc tac atc atc ttg gta gga ttg ctg cat atg gtt cta ctc agc atc | | 147 |
| Ala Tyr Ile Ile Leu Val Gly Leu Leu His Met Val Leu Leu Ser Ile | | |
| 25 | 30 | 35 |
| ccc ttc ttc agc att cct gtt gtc tgg acc ctg acc aac gtc atc cat | | 195 |
| Pro Phe Phe Ser Ile Pro Val Val Trp Thr Leu Thr Asn Val Ile His | | |
| 45 | 50 | 55 |
| aac ctg gct acg tat gtc ttc ctt cat acg gtg aaa ggg aca ccc ttt | | 243 |
| Asn Leu Ala Thr Tyr Val Phe Leu His Thr Val Lys Gly Thr Pro Phe | | |
| 60 | 65 | 70 |
| gag act cct gac caa gga aag gct cgg cta ctg aca cac tgg gag caa | | 291 |
| Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His Trp Glu Gln | | |
| 75 | 80 | 85 |
| atg gac tat ggg ctc cag ttt acc tct tcc cgc aag ttc ctc agc atc | | 339 |
| Met Asp Tyr Gly Leu Gln Phe Thr Ser Ser Arg Lys Phe Leu Ser Ile | | |
| 90 | 95 | 100 |
| tct cct att gtg ctc tat ctc ctg gcc agc ttc tat acc aag tat gat | | 387 |
| Ser Pro Ile Val Leu Tyr Leu Leu Ala Ser Phe Tyr Thr Lys Tyr Asp | | |
| 105 | 110 | 115 |
| gct gcg cac ttc ctc atc aac aca gcc tca ttg cta agt gta ctg ctg | | 435 |
| Ala Ala His Phe Leu Ile Asn Thr Ala Ser Leu Leu Ser Val Leu Leu | | |
| 125 | 130 | 135 |

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ccg aag ttg ccc cag ttc cat ggg gtt cgt gtc ttt ggc atc aac aaa 483

Pro Lys Leu Pro Gln Phe His Gly Val Arg Val Phe Gly Ile Asn Lys

140

145

150

tac tgag ggatgggttt tgggacagct ccatgggcat ggggaaggca ctgaaacaga 540

Tyr

ggactataaaa acatccttct cttattctcc 570

<210> 23

<211> 1161

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (278)... (880)

<400> 23

acatgagcca ccaaaatggt ggtgttcggg tatgaggctg ggactaagcc aagggtatca 60

ggtgtggtgc cggtgggaac tgaggaagcg cccaaggaaa tgaaacacga tttccaaat 120

gaacttaatc tttcatgaga aactgaggat agagatgtca ataagcagcc actgtttcca 180

cctccccacc tgaagagcta ggaggacaac taaaagagc ctgactgcct tctcggaatg 240

aggagagagg aaaacagcaa cagtatcagt tttcaag atg gca gca tct atg 292

Met Ala Ala Ser Met

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| | |
|---|-----|
| cat ggt cag ccc agt cct tct cta gaa gat gca aaa ctc aga aga cca | 340 |
| His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala Lys Leu Arg Arg Pro | |
| 10 15 20 | |
| atg gtc ata gaa atc ata gaa aaa aat ttt gac tat ctt aga aaa gaa | 388 |
| Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp Tyr Leu Arg Lys Glu | |
| 25 30 35 | |
| atg aca caa aat ata tat caa atg gcg aca ttt gga aca aca gct ggt | 436 |
| Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe Gly Thr Thr Ala Gly | |
| 40 45 50 | |
| ttc tct gga ata ttc tca aac ttc ctg ttc aga cgc tgc ttc aag gtt | 484 |
| Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg Arg Cys Phe Lys Val | |
| 55 60 65 | |
| aaa cat gat gct ttg aag aca tat gca tca ttg gct aca ctt cca ttt | 532 |
| Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu Ala Thr Leu Pro Phe | |
| 70 75 80 85 | |
| ttg tct act gtt gtt act gac aag ctt ttt gta att gat gct ttg tat | 580 |
| Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val Ile Asp Ala Leu Tyr | |
| 90 95 100 | |
| tca gat aat ata agc aag gaa aac tgt gtt ttc aga agc tca ctg att | 628 |
| Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe Arg Ser Ser Leu Ile | |
| 105 110 115 | |
| ggc ata gtt tgt ggt gtt ttc tat ccc agt tct ttg gct ttt act aaa | 676 |
| Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser Leu Ala Phe Thr Lys | |
| 120 125 130 | |
| aat gga cgc ctg gca acc aag tat cat acc gtt cca ctg cca cca aaa | 724 |

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Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val Pro Leu Pro Pro Lys
 135 140 145
 gga agg gtt tta atc cat tgg atg acg ctt tgt caa aca caa atg aaa 772
 Gly Arg Val Leu Ile His Trp Met Thr Leu Cys Gln Thr Gln Met Lys
 150 155 160 165
 tta atg gcg att cct cta gtc ttt cag att atg ttt gga ata tta aat 820
 Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met Phe Gly Ile Leu Asn
 170 175 180
 ggt cta tac cat tat gca gta ttt gaa gag aca ctt gag aaa act ata 868
 Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr Leu Glu Lys Thr Ile
 185 190 195
 cat gaa gag taaccaaaaa aatgaatggg tgctaactta gcaaaatgaa gtt 920
 His Glu Glu
 200
 tctataaaga ggactcaggc attgctgaaa gagttaaag taactgtgaa caaataattt 980
 gttctgtgcc ttttgctgg tatatagcaa atactcaaaa agtattcaat aattcaatca 1040
 ataaatataa gtttcattt acacgtaaga tacaggcttt atctctgat ggtgtgtcca 1100
 ttttgctgg tatataacag ataataaata tccagtgtca ataaatgtaa caataaaagt 1160
 t 1161

<210> 24

<211> 823

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (58)... (627)

<400> 24

| | |
|---|-----|
| acacacacat ctgcacctca accacagact acacttgctg aactggctcc tggggcc | 57 |
| atg agg ctg tca ctg cca ctg ctg ctg ctg ctg gga gcc tgg gcc | 105 |
| Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Leu Gly Ala Trp Ala | |
| 1 5 10 15 | |
| atc cca ggg ggc ctc ggg gac agg gcg cca ctc aca gcc aca gcc cca | 153 |
| Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro | |
| 20 25 30 | |
| caa ctg gat gat gag gag atg tac tca gcc cac atg ccc gct cac ctg | 201 |
| Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu | |
| 35 40 45 | |
| cgc tgt gat gcc tgc aga gct gtg gct tac cag atg tgg caa aat ctg | 249 |
| Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu | |
| 50 55 60 | |
| gca aag gca gag acc aaa ctt cat acc tca aac tct ggg ggg cgg cgg | 297 |
| Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg | |
| 65 70 75 80 | |
| gag ctg agc gag ttg gtc tac acg gat gtc ctg gac cgg agc tgc tcc | 345 |
| Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Ser Cys Ser | |
| 85 90 95 | |
| cgg aac tgg cag gac tac gga gtt cga gaa gtg gac caa gtg aaa cgt | 393 |

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Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg
 100 105 110
 ctc aca ggc cca gga ctt agc gag ggg cca gag cca agc atc agc gtg 441
 Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val
 115 120 125
 atg gtc aca ggg ggc ccc tgg cct acc agg ctc tcc agg aca tgt ttg 489
 Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu
 130 135 140
 cac tac ttg ggg gag ttt gga gaa gac cag atc tat gaa gcc cac caa 537
 His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln
 145 150 155 160
 caa ggc cga ggg gct ctg gag gca ttg cta tgt ggg gga ccc cag ggg 585
 Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly
 165 170 175
 gcc tgc tca gag aag gtg tca gcc aca aga gaa gag ctc tagtcc 630
 Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu
 180 185
 tggactctac cctcctctga aagaagctgg ggcttgctct gacggctctcc actcccgtct 690
 gcaggcagcc aggagggcag gaagcccttg ctctgtgctg ccacccctgcc tccctcctcc 750
 agcctcaggg cactcgggcc tgggtgggag tcaacgcctt cccctctgga ctcaaataaa 810
 acccagtgc ctc 823